

SEQUENCE LISTING

<110> Reed, John C.
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Roth, Wilfred
Stenner-Liewen, Frank

<120> Novel Death Domain Proteins

<130> P-LJ 5037

<150> 60/301,889
<151> 2001-06-29

<150> 09/715,893
<151> 2000-11-17

<160> 62

<170> FastSEQ for Windows Version 4.0

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<213> Homo sapien

<220>
<221> CDS
<222> (1)...(210)

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Leu Trp Gly Arg Thr Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala
1 5 10 15

ccc gag gaa tta gca ctt gtt cac aac ttg agg aaa atg atg aaa aat 96
Pro Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn
20 25 30

gat tgg cat gga ggc gcc att gtg tcg gct ttg agc cag act ggg tct 144
Asp Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser
35 40 45

ctc ttt aag ccc cgg aaa gcc tat ctg ccc cag gag ttg ctg gga aag 192
Leu Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys
50 55 60

gaa gga ttt gat gcc ctg 210
Glu Gly Phe Asp Ala Leu
65 70

<210> 2
 <211> 70
 <212> PRT
 <213> Homo sapien

<400> 2
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 1 5 10 15
 Pro Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn
 20 25 30
 Asp Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser
 35 40 45
 Leu Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys
 50 55 60
 Glu Gly Phe Asp Ala Leu
 65 70

<210> 3
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 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(297)

<400> 3
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 Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly Glu Lys
 1 5 10 15

gga aca gga aaa acc cta agt ctt tgc cat gtt att cat ttc tgt gca 96
 Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe Cys Ala
 20 25 30

aaa cag gac tgg ctg ata cta cat att cca gat gct cat ctt tgg gtg 144
 Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu Trp Val
 35 40 45

aaa aat tgt cgg gat ctt ctg cag tcc agc tac aac aaa cag cgc ttt 192
 Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln Arg Phe
 50 55 60

gat caa cct tta gag gct tca acc tgg ctg aag aat ttc aaa act aca 240
 Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys Thr Thr
 65 70 75 80

aat gag cgc ttc ctg aac cag ata aaa gtt caa gag aag tat gtc tgg 288
 Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr Val Trp
 85 90 95

aat aag aga 297

Asn Lys Arg

<210> 4
<211> 99
<212> PRT
<213> Homo sapien

<400> 4

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	20					25						30			
Lys	Gln	Asp	Trp	Leu	Ile	Leu	His	Ile	Pro	Asp	Ala	His	Leu	Trp	Val
	35					40				45					
Lys	Asn	Cys	Arg	Asp	Leu	Leu	Gln	Ser	Ser	Tyr	Asn	Lys	Gln	Arg	Phe
	50					55			60						
Asp	Gln	Pro	Leu	Glu	Ala	Ser	Thr	Trp	Leu	Lys	Asn	Phe	Lys	Thr	Thr
	65					70			75			80			
Asn	Glu	Arg	Phe	Leu	Asn	Gln	Ile	Lys	Val	Gln	Glu	Lys	Tyr	Val	Trp
					85				90			95			

Asn Lys Arg

<210> 5
<211> 294
<212> DNA
<213> Homo sapien

<220>

<221> CDS

<222> (1)...(294)

<400> 5

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1					5					10			15		

ttt att gat cct caa gaa gga tgg aag aag tta gct gta gct att aaa 96

Phe	Ile	Asp	Pro	Gln	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Val	Ala	Ile	Lys
						20			25			30			

aaa cca tct ggt gat aga tac aat cag ttt cac ata agg aga ttt 144

Lys	Pro	Ser	Gly	Asp	Asp	Arg	Tyr	Asn	Gln	Phe	His	Ile	Arg	Arg	Phe
					35			40			45				

gaa gca tta ctt caa act gga aaa agt ccc act tct gaa tta ctg ttt 192

Glu	Ala	Leu	Leu	Gln	Thr	Gly	Lys	Ser	Pro	Thr	Ser	Glu	Leu	Leu	Phe
					50			55		60					

gac tgg ggc acc aca aat tgc aca gtt ggt gat ctt gtg gat ctt ttg 240

Asp	Trp	Gly	Thr	Thr	Asn	Cys	Thr	Val	Gly	Asp	Leu	Val	Asp	Leu	Leu
					65			70		75		80			

atc caa aat gaa ttt ttt gct cct gcg agt ctt ttg ctc cca gat gct 288
Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu Leu Leu Pro Asp Ala
85 90 95

gtt ccc 294
Val Pro

<210> 6
<211> 98
<212> PRT
<213> Homo sapien

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Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu Ala Val Ala Ile Lys
20 25 30
Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe His Ile Arg Arg Phe
35 40 45
Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr Ser Glu Leu Leu Phe
50 55 60
Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp Leu Val Asp Leu Leu
65 70 75 80
Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu Leu Leu Pro Asp Ala
85 90 95
Val Pro

<210> 7
<211> 303
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(303)

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Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His
1 5 10 15

cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc gag ctg gag 96
Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu
20 25 30

ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc gga ggc tta 144
Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu
35 40 45

gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg gag cgc cgc 192

Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Glu Leu Glu Arg Arg			
50	55	60	
ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc			240
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg			
65	70	75	80
gtg ctg gcc cgc cac gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc			288
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg			
85	90	95	
cgg cca gtg tct cca			303
Arg Pro Val Ser Pro			
100			

<210> 8
<211> 101
<212> PRT
<213> Homo sapien

<400> 8			
Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His			
1	5	10	15
Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu			
20	25	30	
Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu			
35	40	45	
Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Glu Leu Glu Arg Arg			
50	55	60	
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg			
65	70	75	80
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg			
85	90	95	
Arg Pro Val Ser Pro			
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<210> 9
<211> 195
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(195)

<400> 9			
gat ttg tgg aag cag ttt gtg ttt gct cta gga gtt act cca gaa gag			48
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Thr Pro Glu Glu			
1	5	10	15

tta gag gct cat gag cct agt gaa gca gca aaa gcg aaa gta gct act			96
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr			
20	25	30	

ttc atg cgg tgg tgt aca gga gat tct tta gct gca gga gtg gct gct 144
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
35 40 45

ttg tat tct tat gag agt caa att cca cgt atc gct aga gag aaa att 192
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
50 55 60

cgt 195
Arg
65

<210> 10
<211> 65
<212> PRT
<213> Chlamydia trachomatis

<400> 10
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Thr Pro Glu Glu
1 5 10 15
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
20 25 30
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
35 40 45
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
50 55 60
Arg
65

<210> 11
<211> 213
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(213)

<400> 11
cag cag cag gag gaa gtc cag cgg ctc ctg atg atg ggt gag cca gcc 48
Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
1 5 10 15

aag ggc tgg cag gag ctg gca ggc cac ctc ggc tac caa gct gag gct 96
Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
20 25 30

gtg gaa acc atg gcc tgg gac caa atg cca gcc tat acc ctc cta agg 144
Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
35 40 45

aac tgg gct gcc caa gaa ggc aat aga gct acc ctc aga gtg ctg gag 192

Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
50 55 60

gat gct ctg gct gcc ata ggc 213
Asp Ala Leu Ala Ala Ile Gly
65 70

<210> 12
<211> 71
<212> PRT
<213> Mus musculus

<400> 12
Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
1 5 10 15
Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
20 25 30
Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
35 40 45
Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
50 55 60
Asp Ala Leu Ala Ala Ile Gly
65 70

<210> 13
<211> 1605
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (74) ... (1267)

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ctcacgtgca agg atg atg ctg aaa gga ata aca agg ctt atc tct agg 109
Met Met Leu Lys Gly Ile Thr Arg Leu Ile Ser Arg
1 5 10

atc cat aag ttg gac cct ggg cgt ttt tta cac atg ggg acc cag gag 157
Ile His Lys Leu Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala
15 20 25

cgc caa agc att gct gct cac cta gat aac cag gtt cca gtt gag agt 205
Arg Gln Ser Ile Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser
30 35 40

ccg aga gct att tcc cgc acc aat gag aat gac ccg gcc aag cat ggg 253
Pro Arg Ala Ile Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly
45 50 55 60

gat cag cac gag ggt cag cac tac aac atc tcc ccc cag gat ttg gag 301
Asp Gln His Glu Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu

H
D
D
P
P
P
P
P
P
P
P
P
P
P
P
P

65

70

75

act gta ttt ccc cat ggc ctt cct ctc cgc ttt gtg atg cag gtg aag			349
Thr Val Phe Pro His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys			
80	85	90	
aca ttc agt gaa gct tgc ctg atg gta agg aaa cca gcc cta gaa ctt			397
Thr Phe Ser Glu Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu			
95	100	105	
ctg cat tac ctg aaa aac acc agt ttt gct tat cca gct ata cga tat			445
Leu His Tyr Leu Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr			
110	115	120	
ctt ctg tat gga gag aag gga aca gga aaa acc cta agt ctt tgc cat			493
Leu Leu Tyr Gly Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His			
125	130	135	140
gtt att cat ttc tgt gca aaa cag gac tgg ctg ata cta cat att cca			541
Val Ile His Phe Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro			
145	150	155	
gat gct cat ctt tgg gtg aaa aat tgt cgg gat ctt ctg cag tcc agc			589
Asp Ala His Leu Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser			
160	165	170	
tac aac aaa cag cgc ttt gat caa cct tta gag gct tca acc tgg ctg			637
Tyr Asn Lys Gln Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu			
175	180	185	
aag aat ttc aaa act aca aat gag cgc ttc ctg aac cag ata aaa gtt			685
Lys Asn Phe Lys Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val			
190	195	200	
caa gag aag tat gtc tgg aat aag aga gaa agc act gag aaa ggg agt			733
Gln Glu Lys Tyr Val Trp Asn Lys Arg Glu Ser Thr Glu Lys Gly Ser			
205	210	215	220
cct ctg gga gaa gtg gtt gaa cag ggc ata aca cgg gtg agg aac gcc			781
Pro Leu Gly Glu Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala			
225	230	235	
aca gat gca gtt gga att gtg ctg aaa gag cta aag agg caa agt tct			829
Thr Asp Ala Val Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser			
240	245	250	
ttg ggt atg ttt cac ctc cta gtg gcc gtg gat gga atc aat gct ctt			877
Leu Gly Met Phe His Leu Leu Ala Val Asp Gly Ile Asn Ala Leu			
255	260	265	
tgg gga aga acc act ctg aaa aga gaa gat aaa agc ccg att gcc ccc			925
Trp Gly Arg Thr Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro			
270	275	280	
gag gaa tta gca ctt gtt cac aac ttg agg aaa atg atg aaa aat gat			973

Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp			
285	290	295	300
tgg cat gga ggc gcc att gtg tcg gct ttg agc cag act ggg tct ctc			1021
Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu			
305	310	315	
ttt aag ccc cgaaaaa gcc tat ctg ccc cag gag ttg ctg gga aag gaa			1069
Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu			
320	325	330	
gga ttt gat gcc ctg gat ccc ttt att ccc atc ctg gtt tcc aac tat			1117
Gly Phe Asp Ala Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr			
335	340	345	
aac cca aag gaa ttt gaa agt tgt att cag tat tat ttg gaa aac aat			1165
Asn Pro Lys Glu Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn			
350	355	360	
tgg ctt caa cat gag aaa gct cct aca gaa gaa ggg aaa aaa gag ctg			1213
Trp Leu Gln His Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu			
365	370	375	380
ctg ttc cta agt aac gcg aac ccc tcg ctg ctg gag cgg cac tgt gcc			1261
Leu Phe Leu Ser Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala			
385	390	395	
tac ctc taagccaaga tcacagcatg tgaggaagac agtggacatc tgctttatgc			1317
Tyr Leu			
tggaccagt aagatgagga agtcgggcag tacacagaa gaggagccag gcccattgtac			1377
ctatggatt ggacaggact gcagttggct ctggacctgc attaaaatgg gtttcactgt			1437
gaatgcgtga caataagata ttccttggtt cctaaaactt tatatcagtt tattggatgt			1497
ggttttcac atttaagata attatggctc tttctctaaa aaataaaata tctttctaaa			1557
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			1605
<210> 14			
<211> 398			
<212> PRT			
<213> Homo sapien			
<400> 14			
Met Met Leu Lys Gly Ile Thr Arg Leu Ile Ser Arg Ile His Lys Leu			
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Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala Arg Gln Ser Ile			
20	25	30	
Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser Pro Arg Ala Ile			
35	40	45	
Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly Asp Gln His Glu			
50	55	60	
Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu Thr Val Phe Pro			
65	70	75	80
His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys Thr Phe Ser Glu			
85	90	95	

Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu Leu His Tyr Leu
 100 105 110
 Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly
 115 120 125
 Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe
 130 135 140
 Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu
 145 150 155 160
 Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln
 165 170 175
 Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys
 180 185 190
 Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr
 195 200 205
 Val Trp Asn Lys Arg Glu Ser Thr Glu Lys Gly Ser Pro Leu Gly Glu
 210 215 220
 Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala Thr Asp Ala Val
 225 230 235 240
 Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser Leu Gly Met Phe
 245 250 255
 His Leu Leu Val Ala Val Asp Gly Ile Asn Ala Leu Trp Gly Arg Thr
 260 265 270
 Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro Glu Glu Leu Ala
 275 280 285
 Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp Trp His Gly Gly
 290 295 300
 Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu Phe Lys Pro Arg
 305 310 315 320
 Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu Gly Phe Asp Ala
 325 330 335
 Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr Asn Pro Lys Glu
 340 345 350
 Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn Trp Leu Gln His
 355 360 365
 Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu Leu Phe Leu Ser
 370 375 380
 Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala Tyr Leu
 385 390 395

<210> 15
 <211> 1383
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(1380)

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 Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1 5 10 15

gga cta att agg aag ctg tca gat ttt att gat cct caa gaa gga tgg 96

Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp			
20	25	30	
aag aag tta gct gta gct att aaa aaa cca tct ggt gat gat aga tac			144
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr			
35	40	45	
aat cag ttt cac ata agg aga ttt gaa gca tta ctt caa act gga aaa			192
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys			
50	55	60	
agt ccc act tct gaa tta ctg ttt gac tgg ggc acc aca aat tgc aca			240
Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr			
65	70	75	80
gtt ggt gat ctt gtg gat ctt ttg atc caa aat gaa ttt ttt gct cct			288
Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro			
85	90	95	
gcg agt ctt ttg ctc cca gat gct gtt ccc aaa act gct aat aca cta			336
Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu			
100	105	110	
cct tct aaa gaa gct ata aca gtt cag caa aaa cag atg cct ttc tgt			384
Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys			
115	120	125	
gac aaa gac agg aca ttg atg aca cct gtg cag aat ctt gaa caa agc			432
Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser			
130	135	140	
tat atg cca cct gac tcc tca agt cca gaa aat aaa agt tta gaa gtt			480
Tyr Met Pro Pro Asp Ser Ser Pro Glu Asn Lys Ser Leu Glu Val			
145	150	155	160
agt gat aca cgt ttt cac agt ttt tca ttt tat gaa ttg aag aat gtc			528
Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val			
165	170	175	
aca aat aac ttt gat gaa cga ccc att tct gtt ggt aat aaa atg			576
Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met			
180	185	190	
gga gag gga gga ttt gga gtt gta tat aaa ggc tac gta aat aac aca			624
Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr			
195	200	205	
act gtg gca gtg aag aag ctt gca gca atg gtt gac att act act gaa			672
Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu			
210	215	220	
gaa ctg aaa cag cag ttt gat caa gaa ata aaa gta atg gca aag tgt			720
Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys			
225	230	235	240

caa cat gaa aac tta gta gaa cta ctt ggt ttc tca agt gat gga gat			768
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp			
245	250	255	
gac ctc tgc tta gta tat gtt tac atg cct aat ggt tca ttg cta gac			816
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp			
260	265	270	
aga ctc tct tgc ttg gat ggt act cca cca ctt tct tgg cac atg aga			864
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg			
275	280	285	
tgc aag att gct cag ggt gca gct aat ggc atc aat ttt cta cat gaa			912
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu			
290	295	300	
aat cat cat att cat aga gat att aaa agt gca aat atc tta ctg gat			960
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp			
305	310	315	320
gaa gct ttt act gct aaa ata tct gac ttt ggc ctt gca cggt gct tct			1008
Glu Ala Phe Thr Ala Lys Ser Asp Phe Gly Leu Ala Arg Ala Ser			
325	330	335	
gag aag ttt gcc cag aca gtc atg act agc aga att gtg gga aca aca			1056
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr			
340	345	350	
gct tat atg gca cca gaa gct ttg cgt gga gaa ata aca ccc aaa tct			1104
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser			
355	360	365	
gat att tac agc ttt ggt gtg gtt tta cta gaa ata ata act gga ctt			1152
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu			
370	375	380	
cca gct gtg gat gaa cac cgt gaa cct cag tta ttg cta gat att aaa			1200
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Asp Ile Lys			
385	390	395	400
gaa gaa att gaa gat gaa gaa aag aca att gaa gat tat att gat aaa			1248
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys			
405	410	415	
aag atg aat gat gct gat tcc act tca gtt gaa gct atg tac tct gtt			1296
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val			
420	425	430	
gct agt caa tgt ctg cat gaa aag aaa aat aag aga cca gac att aag			1344
Ala Ser Gln Cys Leu His Glu Lys Lys Asn Lys Arg Pro Asp Ile Lys			
435	440	445	
aag gtt caa cag ctg ctg caa gag atg aca gct tct taa			1383
Lys Val Gln Gln Leu Leu Gln Glu Met Thr Ala Ser			
450	455	460	

<210> 16
<211> 460
<212> PRT
<213> Homo sapien

<400> 16
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
1 5 10 15
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
20 25 30
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
35 40 45
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
50 55 60
Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
65 70 75 80
Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
85 90 95
Ala Ser Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
100 105 110
Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
115 120 125
Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
130 135 140
Tyr Met Pro Pro Asp Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
145 150 155 160
Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
165 170 175
Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
180 185 190
Gly Glu Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
195 200 205
Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
210 215 220
Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
225 230 235 240
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp
245 250 255
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
260 265 270
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
275 280 285
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
290 295 300
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
305 310 315 320
Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
325 330 335
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
340 345 350
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
355 360 365
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu

370	375	380
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys		
385	390	395 400
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys		
405	410	415
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val		
420	425	430
Ala Ser Gln Cys Leu His Glu Lys Lys Asn Lys Arg Pro Asp Ile Lys		
435	440	445
Lys Val Gln Gln Leu Leu Gln Glu Met Thr Ala Ser		
450	455	460

<210> 17
<211> 1924
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (91) ... (1044)

<221> misc_feature
<222> (1) ... (1900)
<223> n = A,T,C or G

<400> 17
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ctgagcttgt tccgcctccc tccccccggga atg gcg cta tcc ggg tcg acc ccg 114
Met Ala Leu Ser Gly Ser Thr Pro
1 5

gcc ccg tgc tgg gag gag gat gag tgc ctg gac tac tac ggg atg ctg 162
Ala Pro Cys Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu
10 15 20

tcg ctt cac cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc 210
Ser Leu His Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys
25 30 35 40

gag ctg gag ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc 258
Glu Leu Glu Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala
45 50 55

gga ggc tta gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg 306
Gly Gly Leu Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Glu Leu
60 65 70

gag cgc cgc ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa 354
Glu Arg Arg Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln
75 80 85

ctc ctg cgc gtg ctg gcc cgc cac gac ctg ctg cgg cac ctg gcg cgc 402
Leu Leu Arg Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg
90 95 100

aag	cgg	cgc	cgg	cca	gtg	tct	cca	gaa	cgc	tat	agc	tat	ggc	acc	tcc		450
Lys	Arg	Arg	Arg	Pro	Val	Ser	Pro	Glu	Arg	Tyr	Ser	Tyr	Gly	Thr	Ser		
105				110				115					120				
agc	tct	tca	aag	agg	aca	gag	ggt	agc	tgc	cgt	cgc	cgt	cgg	cag	tca		498
Ser	Ser	Ser	Lys	Arg	Thr	Glu	Gly	Ser	Cys	Arg	Arg	Arg	Arg	Gln	Ser		
125			130				135										
agc	agt	tct	gca	aat	tct	cag	cag	ggt	cag	tgg	gag	aca	ggc	tcc	ccc		546
Ser	Ser	Ser	Ala	Asn	Ser	Gln	Gln	Gly	Gln	Trp	Glu	Thr	Gly	Ser	Pro		
140			145				150										
cca	acc	aag	cgg	cag	cgg	cgg	agt	cgg	ggc	ccc	agt	ggt	ggt	gcc		594	
Pro	Thr	Lys	Arg	Gln	Arg	Arg	Ser	Arg	Gly	Arg	Pro	Ser	Gly	Gly	Ala		
155			160				165										
aga	cgg	cgg	cgg	aga	ggg	gcc	cca	gcc	ccc	cag	cag	cag	tca	gag		642	
Arg	Arg	Arg	Arg	Gly	Ala	Pro	Ala	Ala	Pro	Gln	Gln	Gln	Ser	Glu			
170			175				180										
ccc	gcc	aga	cct	tcc	tct	gaa	ggc	aaa	gtg	acc	tgt	gac	atc	cgg	ctc		690
Pro	Ala	Arg	Pro	Ser	Ser	Glu	Gly	Lys	Val	Thr	Cys	Asp	Ile	Arg	Leu		
185			190				195						200				
cgg	gtt	cga	gca	gag	tac	tgc	gag	cat	ggg	cca	gcc	ttg	gag	cag	ggc		738
Arg	Val	Arg	Ala	Glu	Tyr	Cys	Glu	His	Gly	Pro	Ala	Leu	Glu	Gln	Gly		
205			210				215										
gtg	gca	tcc	cgg	cgg	ccc	cag	gcg	ctg	gcg	cgg	cag	ctg	gac	gtg	ttt		786
Val	Ala	Ser	Arg	Pro	Gln	Ala	Leu	Ala	Arg	Gln	Leu	Asp	Val	Phe			
220			225				230										
ggg	cag	gcc	acc	gca	gtg	ctg	cgc	tca	agg	gac	ctg	ggc	tct	gtg	gtt		834
Gly	Gln	Ala	Thr	Ala	Val	Leu	Arg	Ser	Arg	Asp	Leu	Gly	Ser	Val	Val		
235			240				245										
tgt	gac	atc	aag	ttc	tca	gag	ctc	tcc	tat	ctg	gac	gcc	ttc	tgg	ggc		882
Cys	Asp	Ile	Lys	Phe	Ser	Glu	Leu	Ser	Tyr	Leu	Asp	Ala	Phe	Trp	Gly		
250			255				260										
gac	tac	ctg	agt	ggc	gcc	ctg	ctg	cag	gcc	ctg	cg	ggc	gt	ttc	ctg		930
Asp	Tyr	Leu	Ser	Gly	Ala	Leu	Leu	Gln	Ala	Leu	Arg	Gly	Val	Phe	Leu		
265			270				275						280				
act	gag	gcc	ctg	cga	gag	gct	gtg	ggc	cgg	gag	gct	gtt	cgc	ctg	ctg		978
Thr	Glu	Ala	Leu	Arg	Glu	Ala	Val	Gly	Arg	Glu	Ala	Val	Arg	Leu	Leu		
285			290				295										
gtc	agt	gtg	gat	gag	gct	gac	tat	gag	gct	ggc	cgg	cgc	cgc	ctg	ttg		1026
Val	Ser	Val	Asp	Glu	Ala	Asp	Tyr	Glu	Ala	Gly	Arg	Arg	Arg	Leu	Leu		
300			305				310										
ctg	atg	gag	gag	gaa	ggg	gggcggcgcc	cgacagaggc	ctcctgatcc								1074	
Leu	Met	Glu	Glu	Gly													

aggactggca ggattgatcc cacctccaag tctccgggcc accttctcct gggaggacga 1134
 ccatctctac cccttagagga ctgtcaact agcatcttg aggactgcga caggaccggg 1194
 acagcaggcc ccttgacagc ccctcccaca ggatgtggc tctgaggcct aaaccattc 1254
 cagctgagtt tccttccag actcctccta ccccgagggt gccccattcg cctccggacg 1314
 cgccggctgg gcctgtatct cagaagggag gggcacagct acacactcac caaaggcccc 1374
 cctgcacatt gtatctctga tcttgggctg tttgcactgt cacaggtgca cacactcgct 1434
 catgctcaca ctgcccctgc tgagatctc ctgggcctc gccctggcct gttcccagca 1494
 cacactttt tggectaagg gttctttt caggacctt aatttgcaca ccaacccaaa 1554
 ctggggtttc agccaaaatc agtgggcact ggagctggg tgcacatggg gcctgctcac 1614
 cttgcccaca nattccagc cagccaggc cctgcccagc ttcaatttac agacctgact 1674
 ntccctcacct tccccctgc tgtccagagc tgaacataga cttgcacttg gatgtcacct 1734
 ggagtgtcac atgggagtgt tatggcagca tcataccaag gcctactgtt gcacatggg 1794
 cccaaaccag taaacagcca cctnttgga aaggaaatgc aaaggcttg ggggtgatgg 1854
 aaaagacctt ttacaaatga taccaattaa actgccctgg aaaggcata ggtggcaaa 1914
 aaaaaaaaaa 1924

<210> 18
 <211> 318
 <212> PRT
 <213> Homo sapien

<400> 18
 Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp Glu
 1 5 10 15
 Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
 20 25 30
 Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe Leu
 35 40 45
 Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
 50 55 60
 Gly Leu Glu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Asp Glu
 65 70 75 80
 Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
 85 90 95
 Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
 100 105 110
 Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Lys Arg Thr Glu Gly
 115 120 125
 Ser Cys Arg Arg Arg Gln Ser Ser Ser Ala Asn Ser Gln Gln
 130 135 140
 Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
 145 150 155 160
 Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Gly Ala Pro
 165 170 175
 Ala Ala Pro Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly
 180 185 190
 Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu
 195 200 205
 His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala
 210 215 220
 Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg
 225 230 235 240
 Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu

245	250	255
Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu		
260	265	270
Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val		
275	280	285
Gly Arg Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp Tyr		
290	295	300
Glu Ala Gly Arg Arg Leu Leu Leu Met Glu Glu Glu Gly		
305	310	315

<210> 19
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(693)

<400> 19		
atg atg gag gtg ttt atg aat ttt tta gat cag tta gat tta att att		48
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile		
1	5	10
		15
caa aat aag cat atg cta gaa cac acg ttt tat gtg aaa tgg tcg aag		96
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys		
20	25	30
ggg gag ctt act aaa gag caa tta cag gcg tat gcc aaa gac tat tat		144
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr		
35	40	45
tta cat atc aaa gcc ttt cct aaa tat tta tct gcg att cat agt cgt		192
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg		
50	55	60
tgc gat gat tta gag gcg cgt aag tta ttg tta gat aac ttg atg gat		240
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Asp Asn Leu Met Asp		
65	70	75
80		
gaa gag aac ggt tac cct aat cat att gat ttg tgg aag cag ttt gtg		288
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val		
85	90	95
ttt gct cta gga gtt act cca gaa gag tta gag gct cat gag cct agt		336
Phe Ala Leu Gly Val Thr Pro Glu Leu Glu Ala His Glu Pro Ser		
100	105	110
gaa gca gca aaa gcg aaa gta gct act ttc atg cgg tgg tgt aca gga		384
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly		
115	120	125
gat tct tta gct gca gga gtg gct ttg tat tct tat gag agt caa		432
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln		

130

135

140

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att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt 480
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145           150           155           160

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gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa 528
 Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
 165 170 175

gcg gat gtg cg^g cat gct aga gaa gaa aaa gc^g ctc att gag atg ctt 576
 Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
 180 185 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg cag gaa gta acg 624
 Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205

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caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca cga act tgt 672
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
      210          215          220

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tgt agt tgt cat caa tct tat taa 696
Cys Ser Cys His Gln Ser Tyr
225 230

<210> 20
<211> 231
<212> PRT
<213> Chlamydia trachomatis

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<400> 20
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
      5           10           15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
      20           25           30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
      35           40           45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
      50           55           60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
      65           70           75           80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
      85           90           95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
      100          105          110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
      115          120          125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
      130          135          140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
      145          150          155           160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
      165          170          175

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Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
 180 185 190
 Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
 195 200 205
 Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
 210 215 220
 Cys Ser Cys His Gln Ser Tyr
 225 230

<210> 21
 <211> 687
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(684)

<400> 21
 atg ctt tat aac gtc agc aaa ggt gtg gtc tat tca gat aca gcc ctg 48
 Met Leu Tyr Asn Val Ser Lys Gly Val Val Tyr Ser Asp Thr Ala Leu
 1 5 10 15

cag ggg cag gac ggg gac agg gaa gga atg tgg gta gga gct ggg gga 96
 Gln Gly Gln Asp Gly Asp Arg Glu Gly Met Trp Val Gly Ala Gly Gly
 20 25 30

gcc cta gcc ccc aat acc tcc tcc cta ttt ccc cct gag cct cca ggg 144
 Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly
 35 40 45

gcc tcg agc aac atc att cct gtc tac tgt gct ctc cta gct aca gtg 192
 Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val
 50 55 60

atc ctt ggt ctg ctg gcc tat gtg gcc ttc aaa tgc tgg cgc tca cat 240
 Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His
 65 70 75 80

aag caa agg caa cag ttg gct aaa gct cgg act gta gag cta ggg gac 288
 Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp
 85 90 95

cct gac agg gac cag agg cgt ggt gac agc aac gtc ttc gtg gac tct 336
 Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser
 100 105 110

cct cct agt ctg gag ccc tgt att ccc agc cag gga cca cac ccg gac 384
 Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp
 115 120 125

ctt ggc tgc cag ctt tac ctg cat att cca cag cag cag cag gag gaa 432
 Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Glu Glu
 130 135 140

gtc cag cgg ctc ctg atg atg ggt gag cca gcc aag ggc tgg cag gag		480	
Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala Lys Gly Trp Gln Glu			
145	150	155	
		160	
ctg gca ggc cac ctc ggc tac caa gct gag gct gtg gaa acc atg gcc		528	
Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala			
165	170	175	
tgt gac caa atg cca gcc tat acc ctg cta agg aac tgg gct gcc caa		576	
Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln			
180	185	190	
gaa ggc aat aga gct acc ctc aga gtg ctg gag gat gct ctg gct gcc		624	
Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Ala Ala			
195	200	205	
ata ggc cga gaa gat gtg gtc cag gtt ttg agc tcg cca gct gag agc		672	
Ile Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Ser			
210	215	220	
tcc tcg gtg gtg tga		687	
Ser Ser Val Val			
225			
<210> 22			
<211> 228			
<212> PRT			
<213> Mus musculus			
<400> 22			
Met Leu Tyr Asn Val Ser Lys Gly Val Val Tyr Ser Asp Thr Ala Leu			
1	5	10	15
Gln Gly Gln Asp Gly Asp Arg Glu Gly Met Trp Val Gly Ala Gly Gly			
20	25		30
Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly			
35	40		45
Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val			
50	55		60
Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His			
65	70	75	80
Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp			
85	90		95
Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser			
100	105		110
Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp			
115	120		125
Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Glu Glu			
130	135		140
Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala Lys Gly Trp Gln Glu			
145	150	155	160
Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala			
165	170		175
Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln			

<210> 23
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1) . . . (693)

<400> 23
atg atg gag gtg ttt atg aat ttt tta gat cag tta gat tta att att 48
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
1 5 10 15

caa aat aag cat atg cta gaa cac aca ttt tat gtg aaa tgg tcg aag 96
 Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
 20 25 30

ggg gag ctt act aaa gag caa tta cag gcg tat gcc aaa gac tat tat 144
 Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
 35 40 45

tta cat atc aaa gcc ttt cct aaa tat tta tct gcg att cat agt cgt 192
 Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
 50 55 60

tgc gat gat tta gag gcg cgt aag tta ttg tta gat aac ttg atg gat	240
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp	
65 70 75 80	

gaa gag aac ggt tac cct aat cat att gat ttg tgg aag cag ttt gtg 288
 Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
 85 90 95

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ttt gct cta gga gtt act cca gaa gag tta gag gag cct agt 336
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
          100           105           110

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gaa gca gca aaa gcg aaa gta gct act ttc atg cg^g tgg tgt aca gga 384
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
115 120 125

gat tct tta gct gca gga gtg gct gct ttg tat tct tat gag agt caa 432 -
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
130 135 140

att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt 480
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145 150 155 160

gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa 528
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
165 170 175

gcg gat gtg cg^g cat gct aga gaa aaa gc^g ctc att gag atg ctt 576
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
180 185 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg caa gaa gta acg 624
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
195 200 205

caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca gga act tgt 672
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
210 215 220

tgt agt tgt cat caa tct tat taa 696
Cys Ser Cys His Gln Ser Tyr
225 230

<210> 24
<211> 231
<212> PRT
<213> Chlamydia trachomatis

<400> 24
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
1 5 10 15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
20 25 30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
35 40 45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
50 55 60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Asp Asn Leu Met Asp
65 70 75 80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
85 90 95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
100 105 110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
115 120 125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
130 135 140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145 150 155 160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
165 170 175
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
180 185 190

Leu	Lys	Asp	Asp	Ala	Asp	Lys	Val	Leu	Glu	Ala	Ser	Gln	Glu	Val	Thr
195						200						205			
Gln	Ser	Leu	Tyr	Gly	Phe	Leu	Asp	Ser	Phe	Leu	Asp	Pro	Gly	Thr	Cys
210						215					220				
Cys	Ser	Cys	His	Gln	Ser	Tyr									
225					230										

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<212> DNA
<213> Homo sapien

<220>
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Met	Asn	Lys	Pro	Ile	Thr	Pro	Ser	Thr	Tyr	Val	Arg	Cys	Leu	Asn	Val
1				5						10				15	48

gga	cta	att	agg	aag	ctg	tca	gat	ttt	att	gat	cct	caa	gaa	gga	tgg
Gly	Leu	Ile	Arg	Lys	Leu	Ser	Asp	Phe	Ile	Asp	Pro	Gln	Glu	Gly	Trp
20					25						30				96

aag	aag	tta	gct	gta	gct	att	aaa	aaa	cca	tct	ggt	gat	gat	aga	tac
Lys	Lys	Leu	Ala	Val	Ala	Ile	Lys	Lys	Pro	Ser	Gly	Asp	Asp	Arg	Tyr
35					40						45				144

aat	cag	ttt	cac	ata	aga	tgc	tgt	tcc	caa	aac	taatacacta	ccttctaaag	197	
Asn	Gln	Phe	His	Ile	Arg	Cys	Cys	Ser	Gln	Asn				
50				55										

aagctataac	agtt													211	
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<210> 26
<211> 59
<212> PRT
<213> Homo sapien

<400>	26														
Met	Asn	Lys	Pro	Ile	Thr	Pro	Ser	Thr	Tyr	Val	Arg	Cys	Leu	Asn	Val
1				5						10			15		
Gly	Leu	Ile	Arg	Lys	Leu	Ser	Asp	Phe	Ile	Asp	Pro	Gln	Glu	Gly	Trp
20					25						30				
Lys	Lys	Leu	Ala	Val	Ala	Ile	Lys	Lys	Pro	Ser	Gly	Asp	Asp	Arg	Tyr
35					40						45				
Asn	Gln	Phe	His	Ile	Arg	Cys	Cys	Ser	Gln	Asn					
50				55											

<210> 27
<211> 2817
<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (50) ... (1429)

<400> 27

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Met Asn Lys
1

ccc ata aca cca tca aca tat gtg cgc tgc ctc aat gtt gga cta att 106
Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile
5 10 15

agg aag ctg tca gat ttt att gat cct caa gaa gga tgg aag aag tta 154
Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu
20 25 30 35

gct gta gct att aaa aaa cca tct ggt gat gat aga tac aat cag ttt 202
Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe
40 45 50

cac ata agg aga ttt gaa gca tta ctt caa act gga aaa agt ccc act 250
His Ile Arg Arg Phe Glu Ala Leu Gln Thr Gly Lys Ser Pro Thr
55 60 65

tct gaa tta ctg ttt gac tgg ggc acc aca aat tgc aca gtt ggt gat 298
Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp
70 75 80

ctt gtg gat ctt ttg atc caa aat gaa ttt ttt gct cct gcg agt ctt 346
Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu
85 90 95

ttg ctc cca gat gct gtt ccc aaa act gct aat aca cta cct tct aaa 394
Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu Pro Ser Lys
100 105 110 115

gaa gct ata aca gtt cag caa aaa cag atg cct ttc tgt gac aaa gac 442
Glu Ala Ile Thr Val Gln Gln Met Pro Phe Cys Asp Lys Asp
120 125 130

agg aca ttg atg aca cct gtg cag aat ctt gaa caa agc tat atg cca 490
Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser Tyr Met Pro
135 140 145

cct gac tcc tca agt cca gaa aat aaa agt tta gaa gtt agt gat aca 538
Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val Ser Asp Thr
150 155 160

cgt ttt cac agt ttt tca ttt tat gaa ttg aag aat gtc aca aat aac 586
Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val Thr Asn Asn
165 170 175

ttt gat gaa cga ccc att tct gtt ggt aat aaa atg gga gag gga			634
Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met Gly Glu Gly			
180	185	190	195
gga ttt gga gtt gta tat aaa ggc tac gta aat aac aca act gtg gca			682
Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr Thr Val Ala			
200	205	210	
gtg aag aag ctt gca gca atg gtt gac att act act gaa gaa ctg aaa			730
Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu Leu Lys			
215	220	225	
cag cag ttt gat caa gaa ata aaa gta atg gca aag tgt caa cat gaa			778
Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys Gln His Glu			
230	235	240	
aac tta gta gaa cta ctt ggt ttc tca agt gat gga gat gac ctc tgc			826
Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp Asp Leu Cys			
245	250	255	
tta gta tat gtt tac atg cct aat ggt tca ttg cta gac aga ctc tct			874
Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg Leu Ser			
260	265	270	275
tgc ttg gat ggt act cca cca ctt tct tgg cac atg aga tgc aag att			922
Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys Lys Ile			
280	285	290	
gct cag ggt gca gct aat ggc atc aat ttt cta cat gaa aat cat cat			970
Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn His His			
295	300	305	
att cat aga gat att aaa agt gca aat atc tta ctg gat gaa gct ttt			1018
Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu Ala Phe			
310	315	320	
act gct aaa ata tct gac ttt ggc ctt gca cgg gct tct gag aag ttt			1066
Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu Lys Phe			
325	330	335	
gcc cag aca gtc atg act agc aga att gtg gga aca aca gct tat atg			1114
Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met			
340	345	350	355
gca cca gaa gct ttg cgt gga gaa ata aca ccc aaa tct gat att tac			1162
Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr			
360	365	370	
agc ttt ggt gtg gtt tta cta gaa ata ata act gga ctt cca gct gtg			1210
Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val			
375	380	385	
gat gaa cac cgt gaa cct cag tta ttg cta gat att aaa gaa gaa att			1258
Asp Glu His Arg Glu Pro Gln Leu Leu Asp Ile Lys Glu Glu Ile			
390	395	400	

gaa gat gaa gaa aag aca att gaa gat tat att gat aaa aag atg aat		1306
Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys Lys Met Asn		
405	410	415
gat gct gat tcc act tca gtt gaa gct atg tac tct ggt gct agc caa		1354
Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Gly Ala Ser Gln		
420	425	430
tgt cgg cat gaa aag aaa aat aag agc cca gac att aag aag gtt cac		1402
Cys Arg His Glu Lys Lys Asn Lys Ser Pro Asp Ile Lys Lys Val His		
440	445	450
cag ctg ctg caa gag atg aca gct tct taaaacttta ttgaaaaaga		1449
Gln Leu Leu Gln Glu Met Thr Ala Ser		
455	460	
ctcttactt tttatataca cctatctcaa ccatttttt aactgattt tttcctaaat	1509	
attcttcctt accttaaca aggcataggc tggtgcagga cagtggttat taaagcatgg	1569	
gttgaacttc caaaaataaa aaatagagcc accatatcaa cacttagccc tacccattag	1629	
tatcaccccc agttcttaca gtaatccctg agaaaatctcc ttcaaggcatc accaaacaca	1689	
gtttgaaaat tacagggta gaaaaagag cctgggctgt atgtagggtg gaaacactct	1749	
gatctgaagc ccagctgact ccactactaa ttgcgttaa agcttggac atacacttag	1809	
ctgctgtgag ccactaataa cattgggcta atatctgtg tgcttctctg acaggtagtc	1869	
atgaaaatca aatgatgcaa aatataataca agcactttgt aaattgtaaa atgatacaaa	1929	
atttaaagtt tatagagcca gttacaaaat cctattagtc atatatttat agattgtgtt	1989	
cacagcaatc atttaaccac aaataaaaata tcccttgatg atactgccat aatgatatgt	2049	
ccattattag attatgttac atgacaaaagt tgaaggaatt tggcagatgc agttaaggtt	2109	
cctaaacaac tcacttgag actgttggaa gggcctgacc taatccaagt gaacccttg	2169	
caagaagaat tctccctgtt agccttgaag aagtatgtga gagggccaca ttggctaaaa	2229	
cctaaaggtt gcctctagga gatgagaccc accttccagt tgtcagcaag caggaaaaaa	2289	
aaattgggac ctcagttgca accacaagga actgaattct gccaaaaatc tgagtcagct	2349	
tagaagagta ctccaagctt cagatgataa ccacagctg ggctgacacc tggatttcag	2409	
ctttgcatttgc ttctcgtat gagaatctat ctgttctgtg ctggacttct aatataataga	2469	
actgtgagat aatgggtcac attggctgga tgtggggct catacctgtt aatcccagca	2529	
ctttgggagg ccgaggcagg cagatcacct gaggtaaaga gttcaagacc ggcctggcca	2589	
acatggtcaa accccgtctc tactaaaaat acaaaaatta gacgagcgtg gtggtggaca	2649	
cctgttagtcc cagctgttgc ggaggctgag gcaggagact agctggacc agggaggtag	2709	
agttgcagt gagctgagat cgtgccactg cactccagcc tgggtgacag agtgagactc	2769	
catcataaaat aaataaataa ataaatgggt cccattaagc cttaaaaa	2817	

<210> 28
<211> 460
<212> PRT
<213> Homo sapien

<400> 28			
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val			
1	5	10	15
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp			
20	25	30	
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr			
35	40	45	
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys			
50	55	60	

Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
 65 70 75 80
 Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
 85 90 95
 Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
 100 105 110
 Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
 115 120 125
 Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
 130 135 140
 Tyr Met Pro Pro Asp Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
 145 150 155 160
 Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
 165 170 175
 Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
 180 185 190
 Gly Glu Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
 195 200 205
 Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
 210 215 220
 Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
 225 230 235 240
 Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp
 245 250 255
 Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
 260 265 270
 Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
 275 280 285
 Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
 290 295 300
 Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
 305 310 315 320
 Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
 325 330 335
 Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
 340 345 350
 Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
 355 360 365
 Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu
 370 375 380
 Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
 385 390 395 400
 Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys
 405 410 415
 Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Gly
 420 425 430
 Ala Ser Gln Cys Arg His Glu Lys Lys Asn Lys Ser Pro Asp Ile Lys
 435 440 445
 Lys Val His Gln Leu Leu Gln Glu Met Thr Ala Ser
 450 455 460

<210> 29

<211> 142

<212> PRT

<213> Homo sapien

<400> 29

Lys Leu Lys Gly Glu Pro Gly Trp Val Thr Ile His Gly Met Ala Gly
1 5 10 15
Cys Gly Lys Ser Val Leu Ala Ala Glu Ala Val Arg Asp His Ser Leu
20 25 30
Leu Glu Gly Cys Phe Pro Gly Gly Val His Trp Val Ser Val Gly Lys
35 40 45
Gln Asp Lys Ser Gly Leu Leu Met Lys Leu Gln Asn Leu Cys Thr Arg
50 55 60
Leu Asp Gln Asp Glu Ser Phe Ser Gln Arg Leu Pro Leu Asn Ile Glu
65 70 75 80
Glu Ala Lys Asp Arg Leu Arg Ile Leu Met Leu Arg Lys His Pro Arg
85 90 95
Ser Leu Leu Ile Leu Asp Asp Val Trp Asp Ser Trp Val Leu Lys Ala
100 105 110
Phe Asp Ser Gln Cys Gln Ile Leu Leu Thr Thr Arg Asp Lys Ser Val
115 120 125
Thr Asp Ser Val Met Gly Pro Lys Tyr Val Val Pro Val Glu
130 135 140

<210> 30

<211> 145

<212> PRT

<213> C. elegans

<400> 30

Glu Met Cys Asp Leu Asp Ser Phe Phe Leu Phe Leu His Gly Arg Ala
1 5 10 15
Gly Ser Gly Lys Ser Val Ile Ala Ser Gln Ala Leu Ser Lys Ser Asp
20 25 30
Gln Leu Ile Gly Ile Asn Tyr Asp Ser Ile Val Trp Leu Lys Asp Ser
35 40 45
Gly Thr Ala Pro Lys Ser Thr Phe Asp Leu Phe Thr Asp Ile Leu Leu
50 55 60
Met Leu Lys Ser Glu Asp Asp Leu Leu Asn Phe Pro Ser Val Glu His
65 70 75 80
Val Thr Ser Val Val Leu Lys Arg Met Ile Cys Asn Ala Leu Ile Asp
85 90 95
Arg Pro Asn Thr Leu Phe Val Phe Asp Asp Val Val Gln Glu Glu Thr
100 105 110
Ile Arg Trp Ala Gln Glu Leu Arg Leu Arg Cys Leu Val Thr Thr Arg
115 120 125
Asp Val Glu Ile Ser Asn Ala Ala Ser Gln Thr Cys Glu Phe Ile Glu
130 135 140
Val
145

<210> 31

<211> 75

<212> PRT

<213> Homo sapien

<400> 31
Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
1 5 10 15
Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
20 25 30
Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
35 40 45
Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
50 55 60
Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu
65 70 75

<210> 32
<211> 76
<212> PRT
<213> Homo sapien

<400> 32
His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val Ser
1 5 10 15
Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile Ser
20 25 30
Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile Glu
35 40 45
Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu Lys
50 55 60
Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys
65 70 75

<210> 33
<211> 77
<212> PRT
<213> Homo sapien

<400> 33
Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly
1 5 10 15
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
20 25 30
Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His
35 40 45
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala
50 55 60
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln
65 70 75

<210> 34
<211> 72
<212> PRT
<213> Homo sapien

<400> 34
Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp
1 5 10 15
Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro
20 25 30
Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln
35 40 45
Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys
50 55 60
Thr Val Val Pro Lys Leu Leu Arg
65 70

<210> 35
<211> 77
<212> PRT
<213> Homo sapien

<400> 35
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65 70 75

<210> 36
<211> 99
<212> PRT
<213> Homo sapien

<400> 36
Trp Pro Glu Glu His Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
1 5 10 15
Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
20 25 30
Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
35 40 45
Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
50 55 60
Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
65 70 75 80
Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Arg Arg Arg Ala
85 90 95
Val Cys Pro

<210> 37
<211> 99

<212> PRT
<213> Mus musculus

<400> 37
Trp Pro Glu Glu Arg Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
1 5 10 15
Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
20 25 30
Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
35 40 45
Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
50 55 60
Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
65 70 75 80
Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Lys Arg Arg Ala
85 90 95
Val Cys Pro

<210> 38
<211> 146
<212> PRT
<213> Danio rerio

<400> 38
Trp Glu Glu Thr Glu Cys Leu Ser Tyr Tyr Glu Thr Leu Ser Leu His
1 5 10 15
Glu Ile Phe Glu Ile Val Gly Ser Gln Leu Thr Glu Thr Cys Gly Gly
20 25 30
Glu Val Ala Phe Leu Leu Asp Glu Thr Tyr Pro Gly Lys His Pro Leu
35 40 45
Asp Pro Glu Gly Trp Thr Glu Asp Leu Pro Pro Gly Pro Asp Gly Ser
50 55 60
Pro Gln Ala Asn Thr Pro Cys Pro Arg Leu Leu Lys Ser Trp Gln Arg
65 70 75 80
Met Gln Pro Gln Lys Glu Gly Cys Ser Ile Ala Ser Arg His Arg Pro
85 90 95
Lys Ser Gly Val Glu Leu Leu Glu Leu Glu Arg Arg Gly Tyr Leu
100 105 110
Ser Asp Ala Asn Leu Arg Pro Leu Leu Gln Leu Leu Arg Ile Leu Thr
115 120 125
Arg His Asp Val Leu Pro Phe Val Ser Gln Lys Lys Arg Arg Thr Val
130 135 140
Ser Pro
145

<210> 39
<211> 82
<212> PRT
<213> Homo sapien

<400> 39
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser

1 5 10 15
Ser Ser Glu Leu Thr Glu Leu Lys Tyr Leu Cys Leu Gly Arg Lys Arg
20 25 30
Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met Leu Leu
35 40 45
Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg Glu Leu
50 55 60
Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp Asp Phe
65 70 75 80
Glu Leu

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 40
atgatgctga aaggaata 18

<210> 41
<211> 40
<212> DNA
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<220>
<223> oligonucleotide

<400> 41
agtccctcgac tcacgtgcaa ggatgatgct gaaaggaaata 40

<210> 42
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 42
gcgaattcat gaacaaaccc ataacaccat caaca 35

<210> 43
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<212> DNA
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<220>
<223> synthetic primer

<400> 43

DNA sequence

gcctcgagtt aagaagctgt catctttgc agcag	35
<210> 44	
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<212> DNA	
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<400> 44	
atgatggagg tgtttatg	18
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<210> 48	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
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<400> 48	

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ccgagggtggc ctgccagctc ctg 23
<210> 49
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 49
acacccggac cttgcctgcc agctttac 28

<210> 50
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 50
atgctttata acgtcagc 18

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 51
tcacaccacc gaggagctct c 21

<210> 52
<211> 195
<212> DNA
<213> C. muridarum

<220>
<221> CDS
<222> (1)...(195)

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Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
1 5 10 15

cta gaa gct cat gaa ccc agt gaa gca gct aaa gct aag gtt gcg aca 96
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
20 25 30

ttt atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct 144
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala

35

40

45

ttg tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att 192
 Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
 50 55 60

cgt 195
 Arg
 65

<210> 53
 <211> 65
 <212> PRT
 <213> C. muridarum

<400> 53
 Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
 1 5 10 15
 Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
 20 25 30
 Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
 35 40 45
 Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
 50 55 60

Arg
 65

<210> 54
 <211> 711
 <212> DNA
 <213> C. muridarum

<220>
 <221> CDS
 <222> (1)...(708)

<400> 54
 atg gaa tca aga aaa gga ata aaa gag gtg agc atg aat ttt tta gat 48
 Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
 1 5 10 15

cag cta gat gca att att caa aac aaa cat atg tta gaa cac cct ttt 96
 Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
 20 25 30

tac atg aag tgg tca aaa gga gag ctg aca aaa gaa caa tta cag gca 144
 Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
 35 40 45

tac gca aaa gat tac tat ttg cat atc aaa gct ttt cca aaa tat tta 192
 Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
 50 55 60

tct gct att cat agc cgt tgt gat gat tta gaa gcc cgc aag tta tta			240
Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu			
65	70	75	80
tta gat aac tta atg gat gaa gag aat ggt tat cct aat cat att gat			288
Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp			
85	90	95	
tta tgg aaa caa ttt gtg ttt gct ctt gga gtg tct tca gaa gag cta			336
Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu			
100	105	110	
gaa gct cat gaa ccc agt gaa gca gct aaa gct aag gtt gcg aca ttt			384
Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe			
115	120	125	
atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct ttg			432
Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu			
130	135	140	
tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att cgt			480
Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg			
145	150	155	160
gga ttg att gag tac ttt ggc ttt tct aat cct gaa gat tat gct tat			528
Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr			
165	170	175	
ttc acg gag cat gaa gaa gct gat gtg cgt cat gct agg gaa gaa aag			576
Phe Thr Glu His Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys			
180	185	190	
gcc tta att gag atg ttg tct aga gat gat agc gac aaa gtt tta gaa			624
Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu			
195	200	205	
gct tcg cga gaa gtt aca caa tct tta tac ggc ttt ttg gat tca ttt			672
Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe			
210	215	220	
tta gag cct gca aca tgt tgt cat tgt cac aaa gct taa			711
Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala			
225	230	235	

<210> 55
<211> 236
<212> PRT
<213> C. muridarum

<400> 55
Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
1 5 10 15
Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
20 25 30

Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
 35 40 45
 Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
 50 55 60
 Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu
 65 70 75 80
 Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp
 85 90 95
 Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu
 100 105 110
 Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe
 115 120 125
 Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu
 130 135 140
 Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg
 145 150 155 160
 Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr
 165 170 175
 Phe Thr Glu His Glu Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys
 180 185 190
 Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu
 195 200 205
 Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe
 210 215 220
 Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala
 225 230 235

<210> 56

<211> 65

<212> PRT

<213> C. pneumoniae

<400> 56

Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly Val Ser Glu Glu Glu
 1 5 10 15
 Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln Asp Met Val Ala Thr
 20 25 30

Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala Val Gly Leu Gly Ala
 35 40 45

Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val Cys Val Glu Lys Ile
 50 55 60

Arg

65

<210> 57

<211> 224

<212> PRT

<213> C. pneumoniae

<400> 57

Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
 1 5 10 15

Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu

20	25	30
Lys Gln Gln Leu Glu Ala Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys		
35	40	45
Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp Asp Leu		
50	55	60
Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu Ala Gly		
65	70	75
Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly		
85	90	95
Val Ser Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln		
100	105	110
Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala		
115	120	125
Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val		
130	135	140
Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val Ser Ala		
145	150	155
Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile Lys His		
165	170	175
Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg Glu Asn		
180	185	190
Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr Leu Trp		
195	200	205
Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser Cys Lys		
210	215	220

<210> 58

<211> 65

<212> PRT

<213> C. psittaci

<400> 58

Asp Leu Trp Lys Asn Phe Ala Tyr Ala Leu Gly Val Thr Glu Glu Glu		
1	5	10
Leu Glu Asn His Val Pro Ser Ala Ala Ala Gln Lys Lys Val Asp Thr		
20	25	30
Phe Leu Arg Trp Cys Thr Gly Asp Ser Leu Ser Ala Gly Val Ala Ala		
35	40	45
Leu Tyr Thr Tyr Glu Ser Gln Ile Pro Thr Val Ala Glu Thr Lys Ile		
50	55	60

Ser

65

<210> 59

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 59

gcagtcatc gcgttggaa

<210> 60
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 60
cgcagaacgg gacataacctt g

21

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 61
tgatatatgcc ggcgtcgtag tc

22

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 62
ggatggcatg ggggagggca ta

22

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